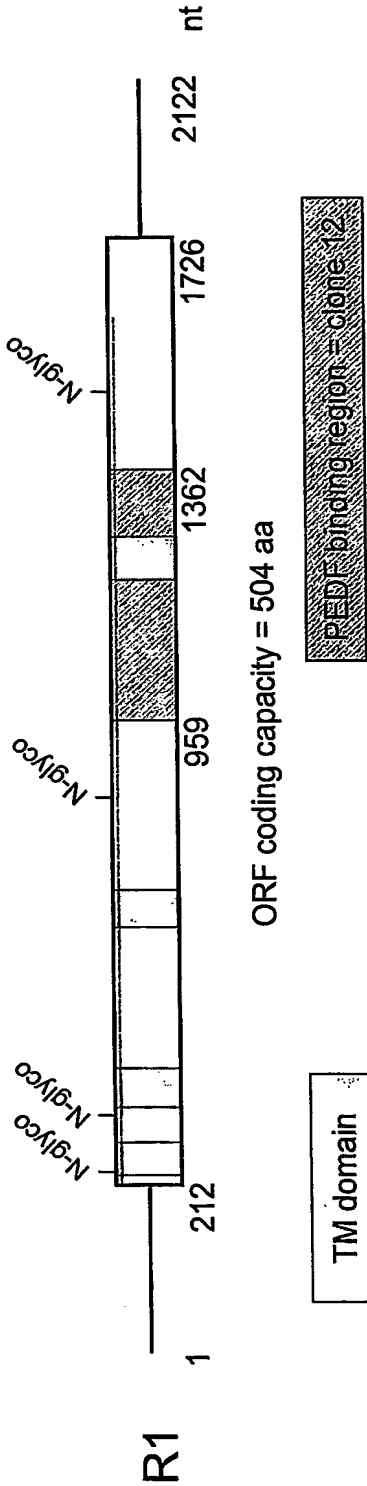
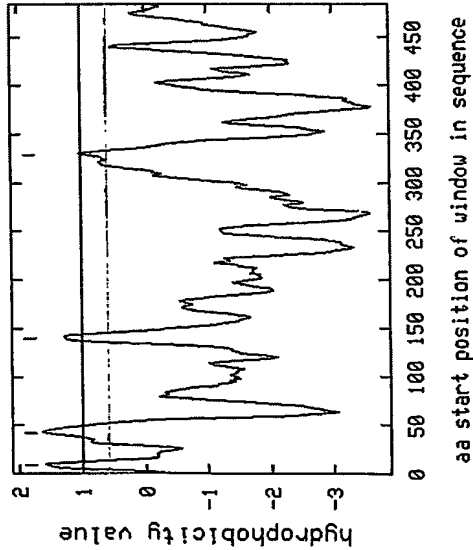


Figure 1.

A.



B.



C.

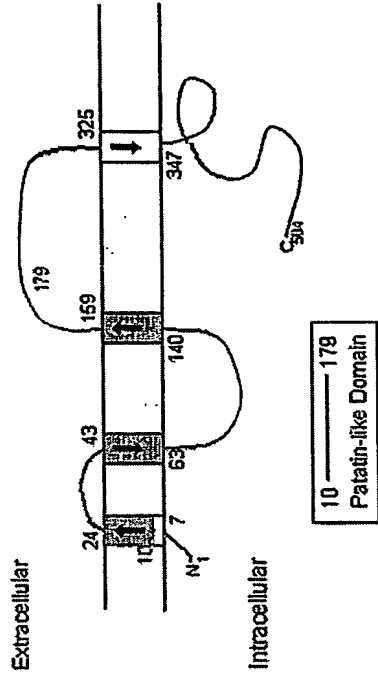


Figure 1.
D.

R1
adiponutrin

MFPREKTNISFAGCGFLGVYTVGVASCLREHAPFLVANATHIYCASAGALTATALTGTGCLGEGAGAKFIEVSKEARKRFLG
YDA RG SL F H ATR H LRD RM LF HCVGVLS I P EQTLQVLSDLVRK S NI

PLHPSFNLVKIIRSFLKVLKVPADSHHEASGRIGLSLTRVSDGENVIISHFNKDELIOANVCSGFTPVYCGGLIPPSLG GVRVY
IF S FL QG C C NV QLI KI LV DFR VVD L C F S FR

DGGISDNLPYELKNTITVSPFSGESDPCQDSSTNIHELVRTNTSIQENLRNLRLSKA LFPPPEPLVLRMCKQGYRDGLR
V V FIDA T P Y Y KVK FLHVDI KL LRLCTG L R FV DLK G I LR L AF

FLQRNGLNRPNP-LLALPP-----ARPHGPEKDQAVESAQAE--DYSQLP--GEDH-ILHHLPARLNEALLE
EEK IC Q G KSSSEGMDPEVAMPSWANNMSLDSS SAAL RLEGD LL HLR SILPW ES DT SP AT S

ACVEPTDLLTTLNMLPVRLATAMVPYTLPLESALSFTIRLLEWLDPVPEDIRWMKEQT GSICQ YLVMRAKRKLGRHLPS
EMKDKGGYMSKIC L I IMSYV L C V IAIQV VT M D VL LQWV SQVFTRVL CLLPASRSQM V

RLPEQVELRRVQSLPS-VPLSCAAAYREALPGWMRNLSIGDALAKWEECQRQLLGLFCTNVAFPPEALMRAPADPAPAPAD
SSQQASPCTPE DW CWT C PKGCPAETKAEATPRSI RSS NFFLGNKVPAGAEGLS --- SFS EKSL-----

PASPQHQLAGPAPLLSTPAPEARPVIGALGL

E.
253 GLLNRPN PLLALPPARP HGEPSKDQAV ESAQAEDYSQ LPGE 293
450 T NVAFPPEARL MRAPADPAPA PADPASPOHQ LAGPAPLLST PAPEARPVIG ALGL 504

Figure 1.**F.**

Homologous patatin phospholipase A (PLA) active site in R1: **S47** and **D166**

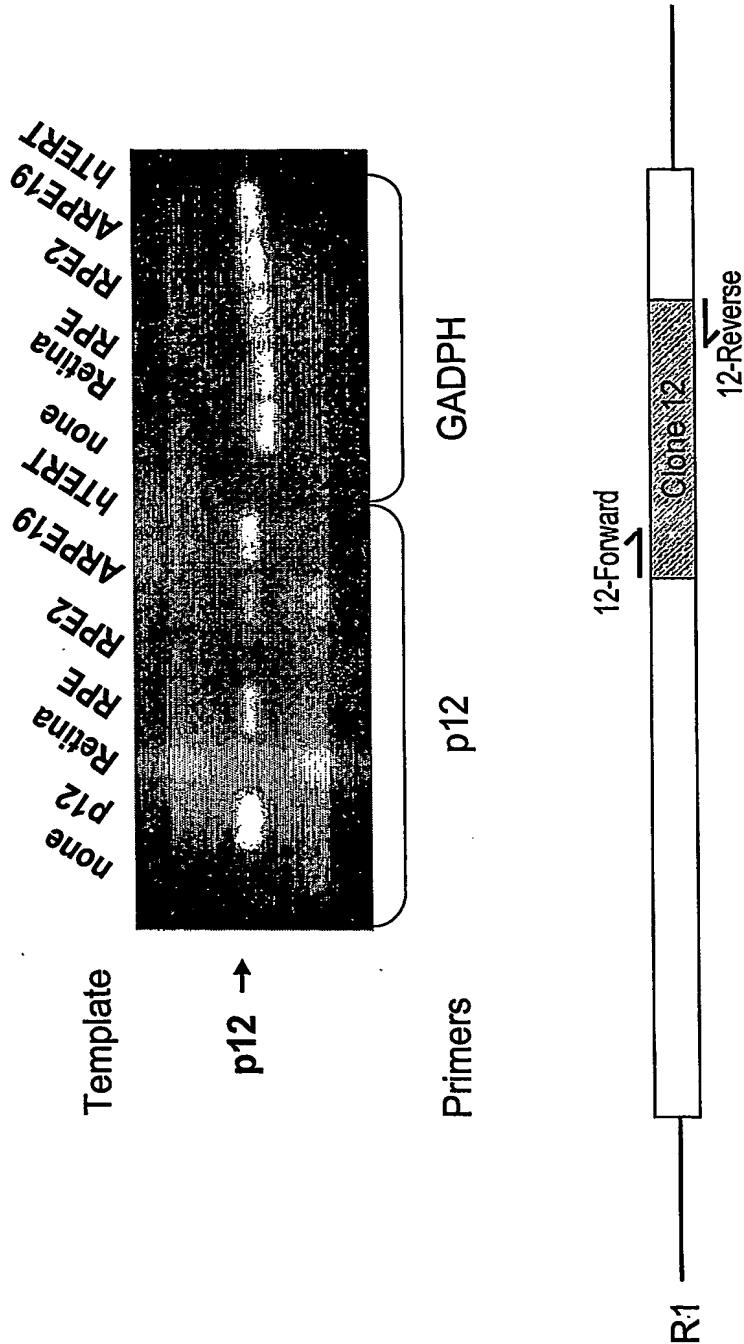
Active site serine

NA	THIYGAS	A	LTA	R1
YF	DVIGGT	S	LTG	Patatin B2
CA	TYVAGL	S	SGST	WYM cPLA2

Active site aspartic

SLQ	GVRVVD	GGIS	DNLPLYE	R1
ARY	EFNLVD	GAVA	TVGDPAL	Patatin B2
KSK	KIHVVVD	SGL-	TFNLPYP	cPLA2

Figure 2.



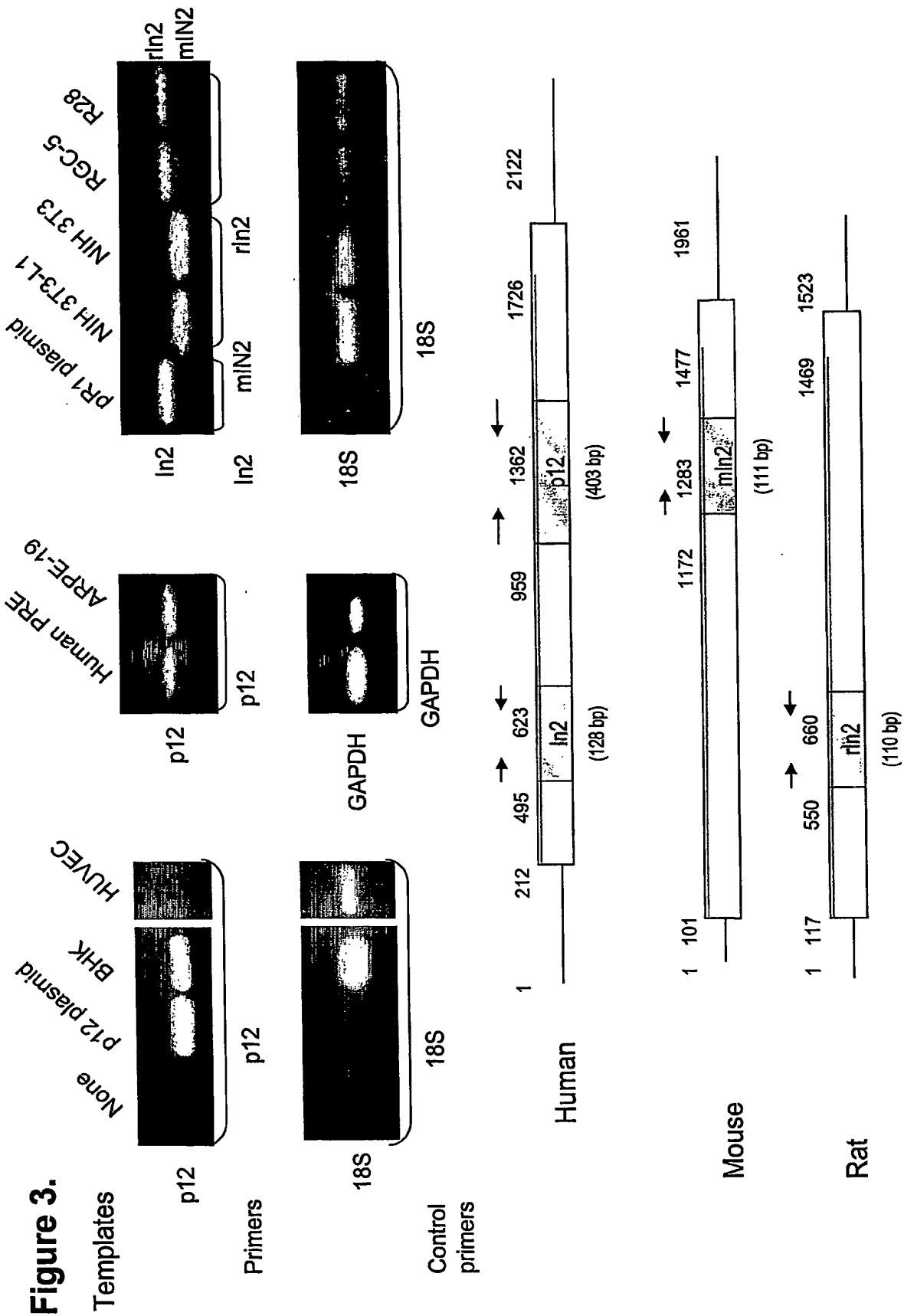


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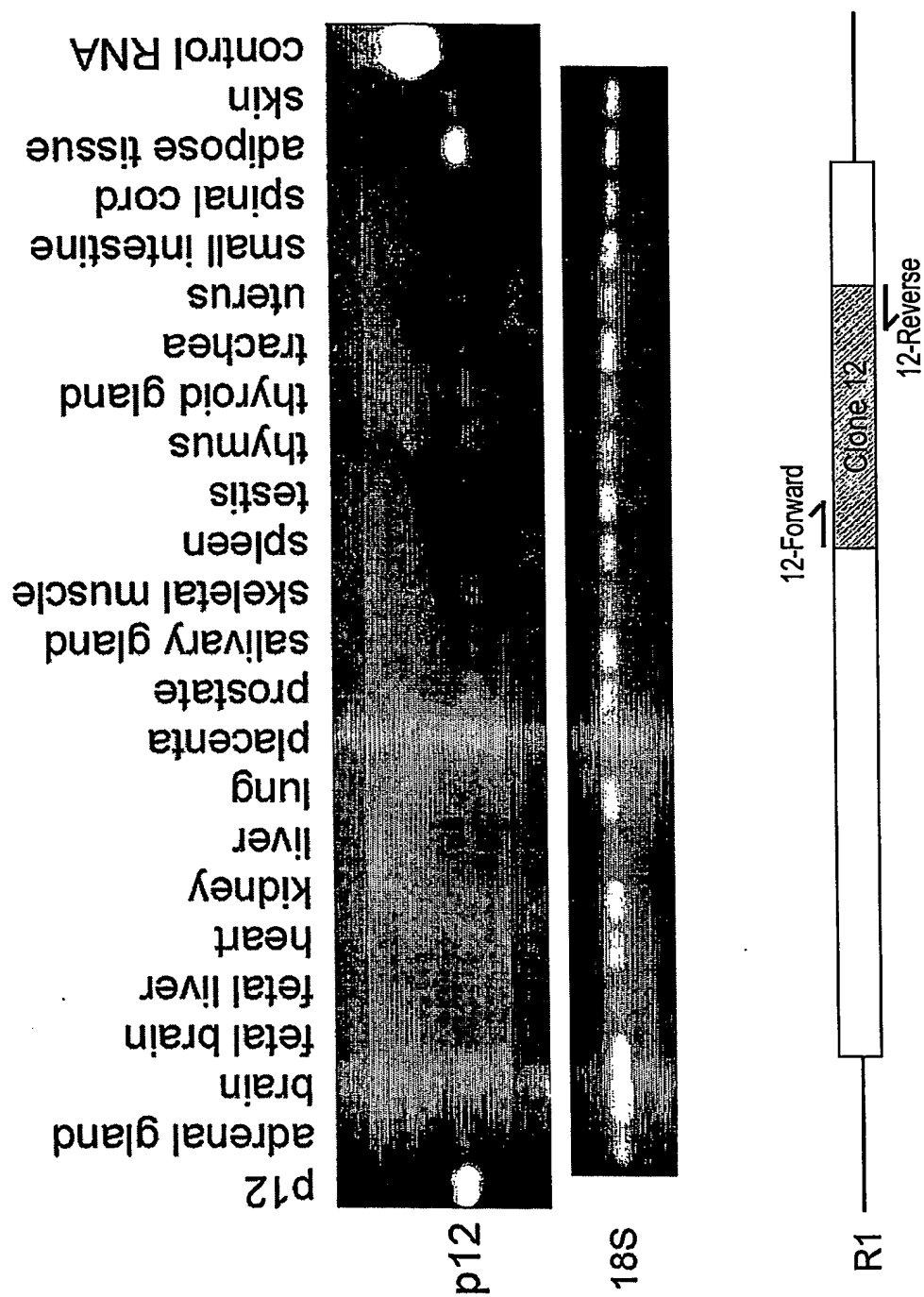
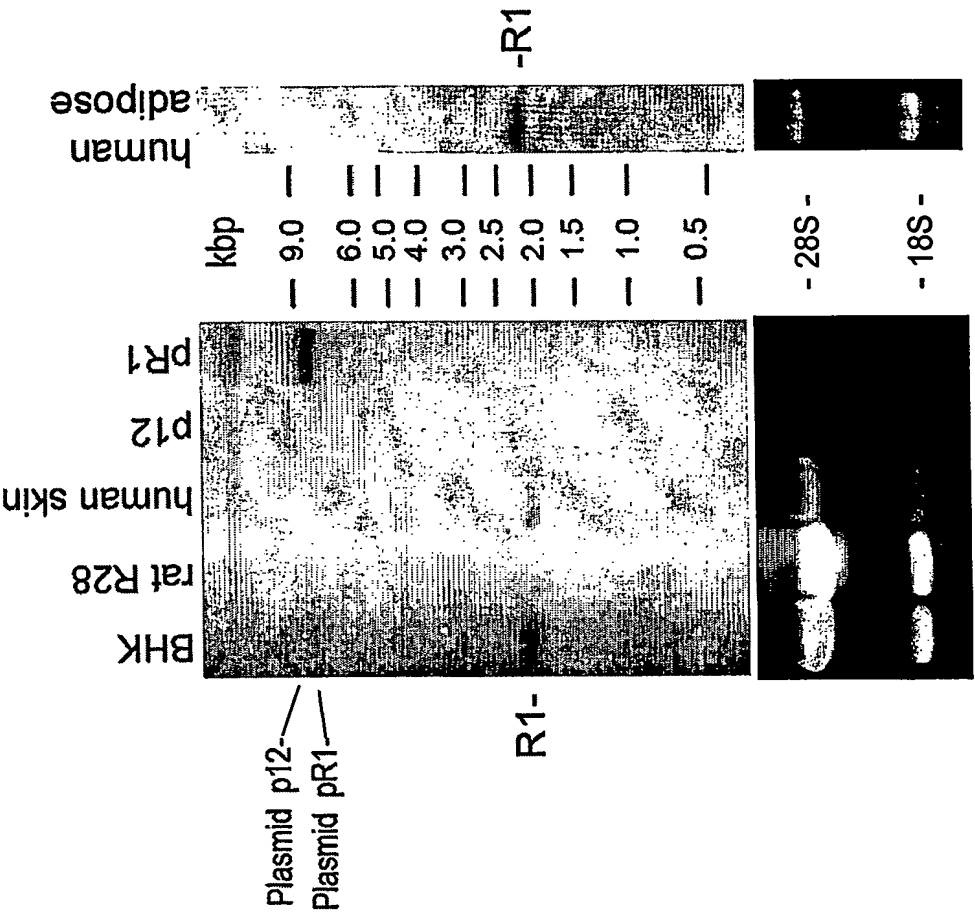


Figure 5.



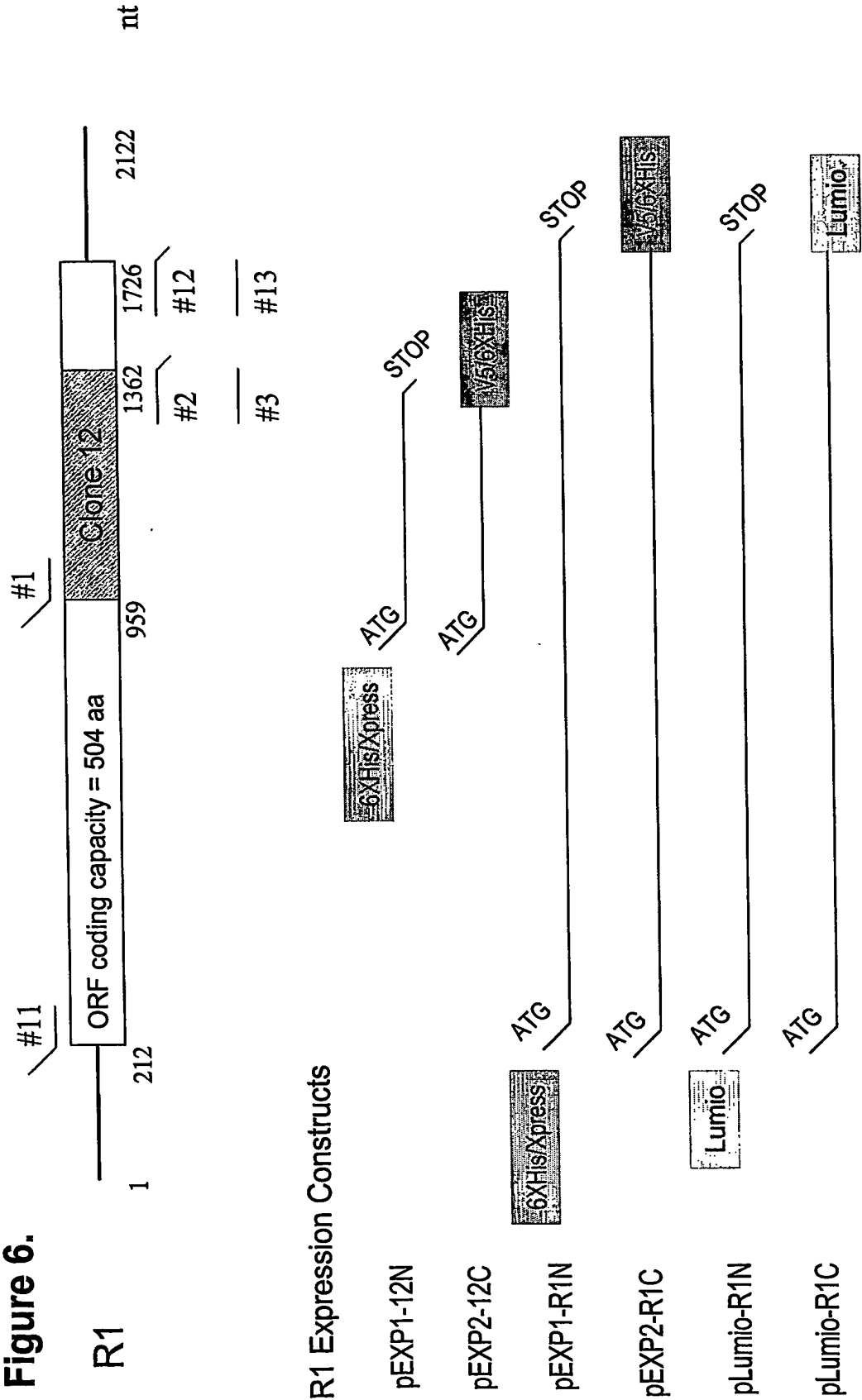
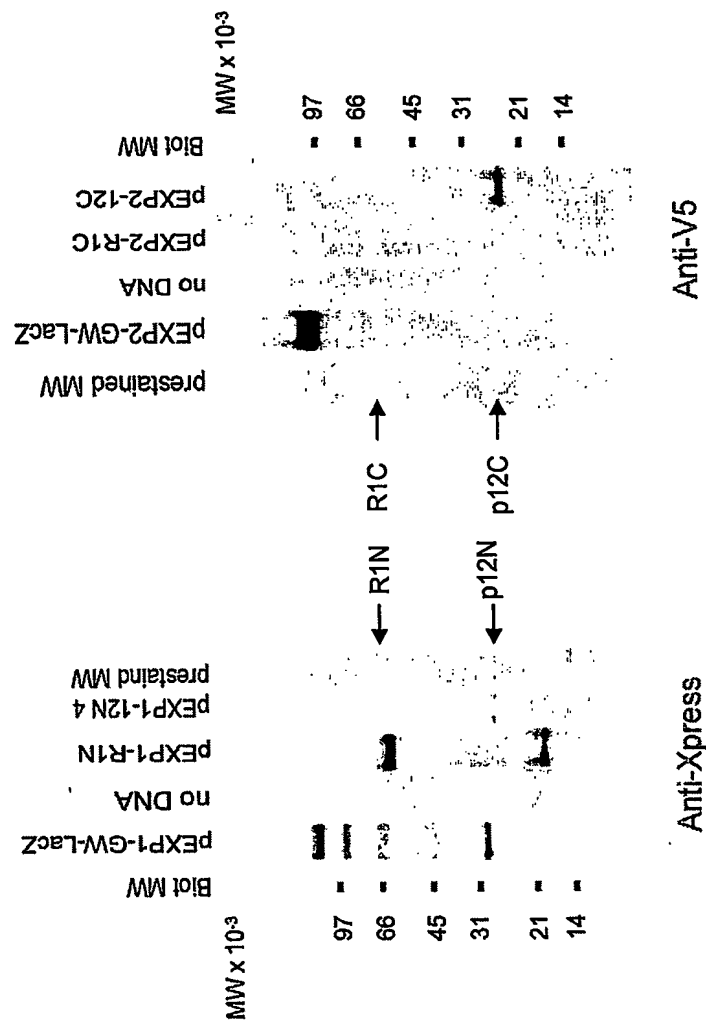


Figure 7.

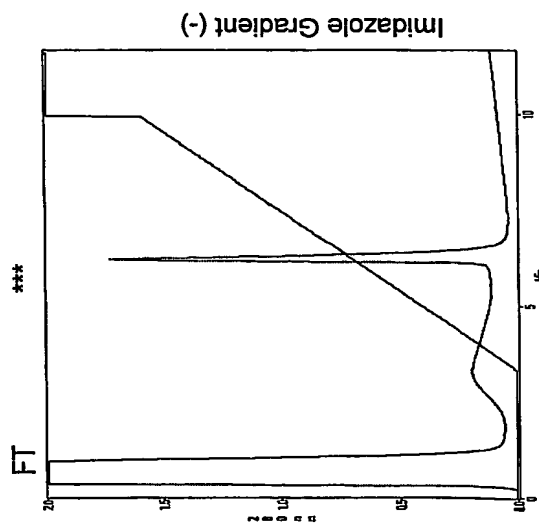


10/30

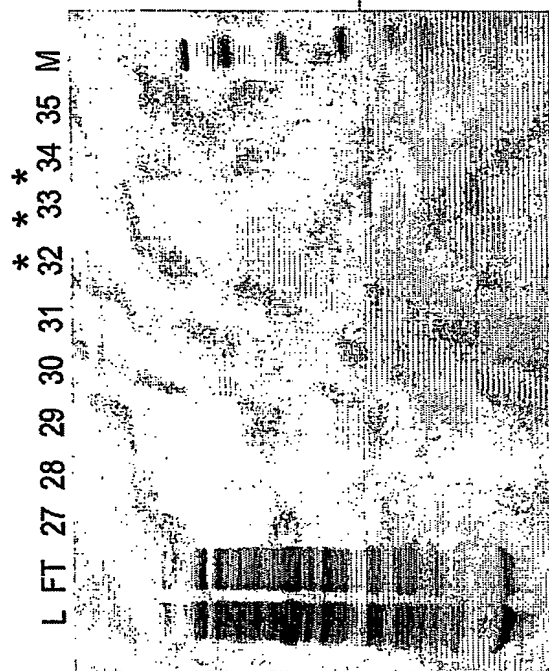
Figure 8.

A. p12

Chromatogram



SDS-PAGE
(Magic Blue stained gel)



Western (Ab-His)

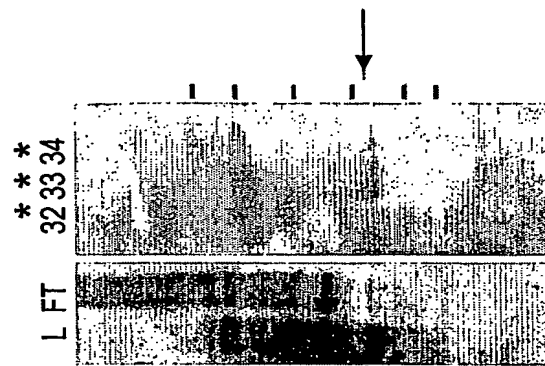
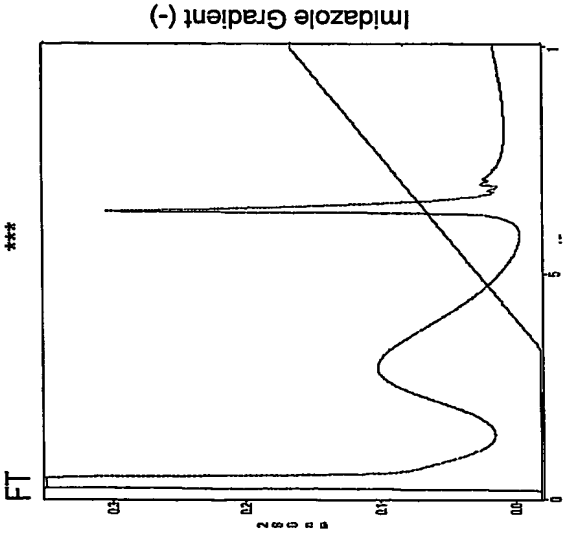


Figure 8.

B. R1

Chromatogram



SDS-PAGE (Coomassie Blue stained gel)

L FT 13 14 15 16 17 18 M

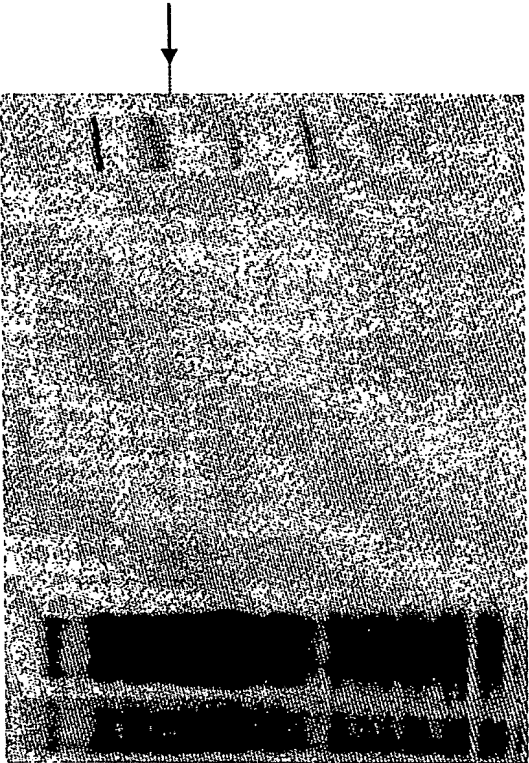
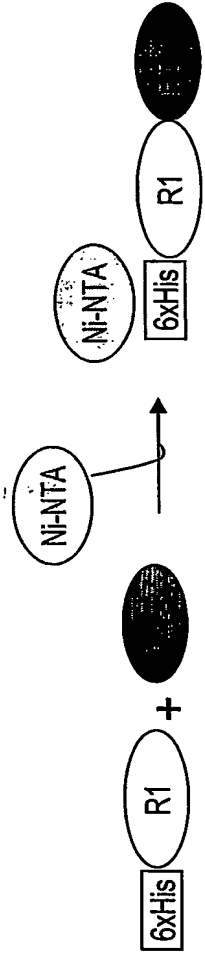


Figure 9.



Figure 10.

A. His-tag pull-down



B. complex formation

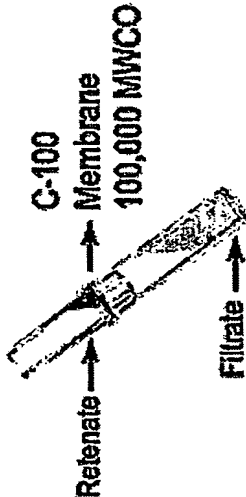
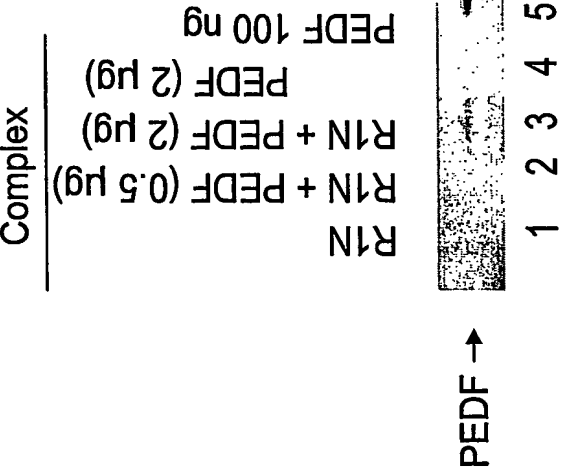
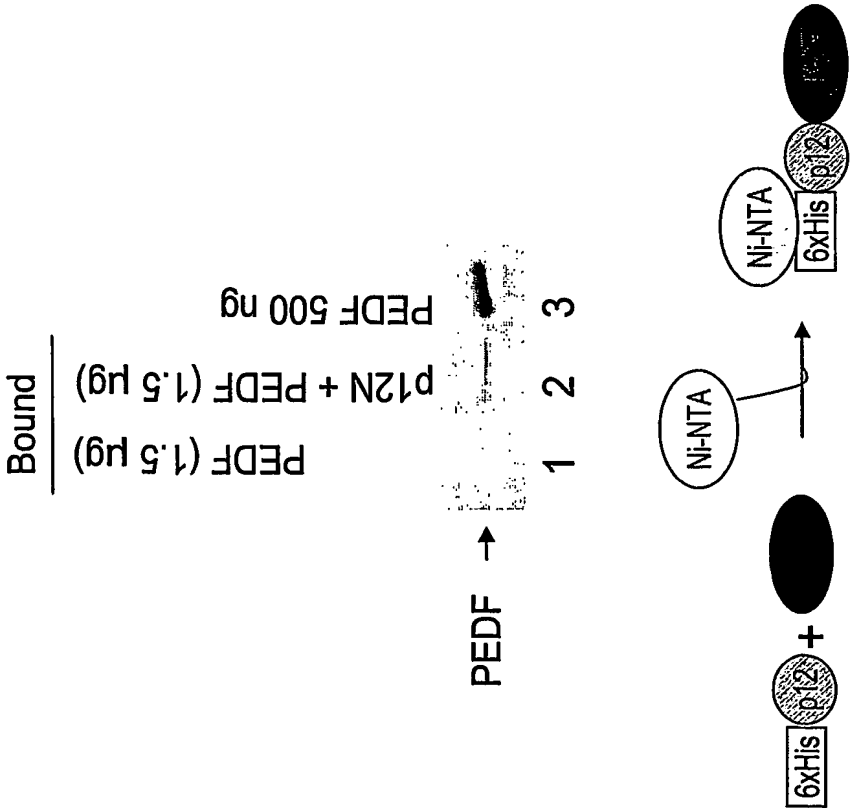


Figure 11.

A.



B.

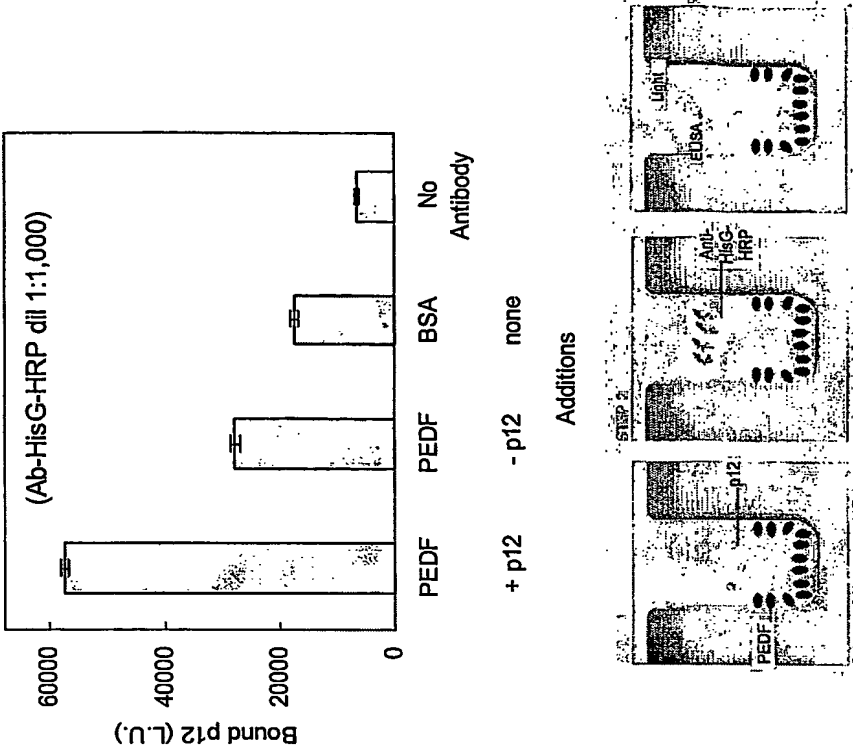


Figure 12.

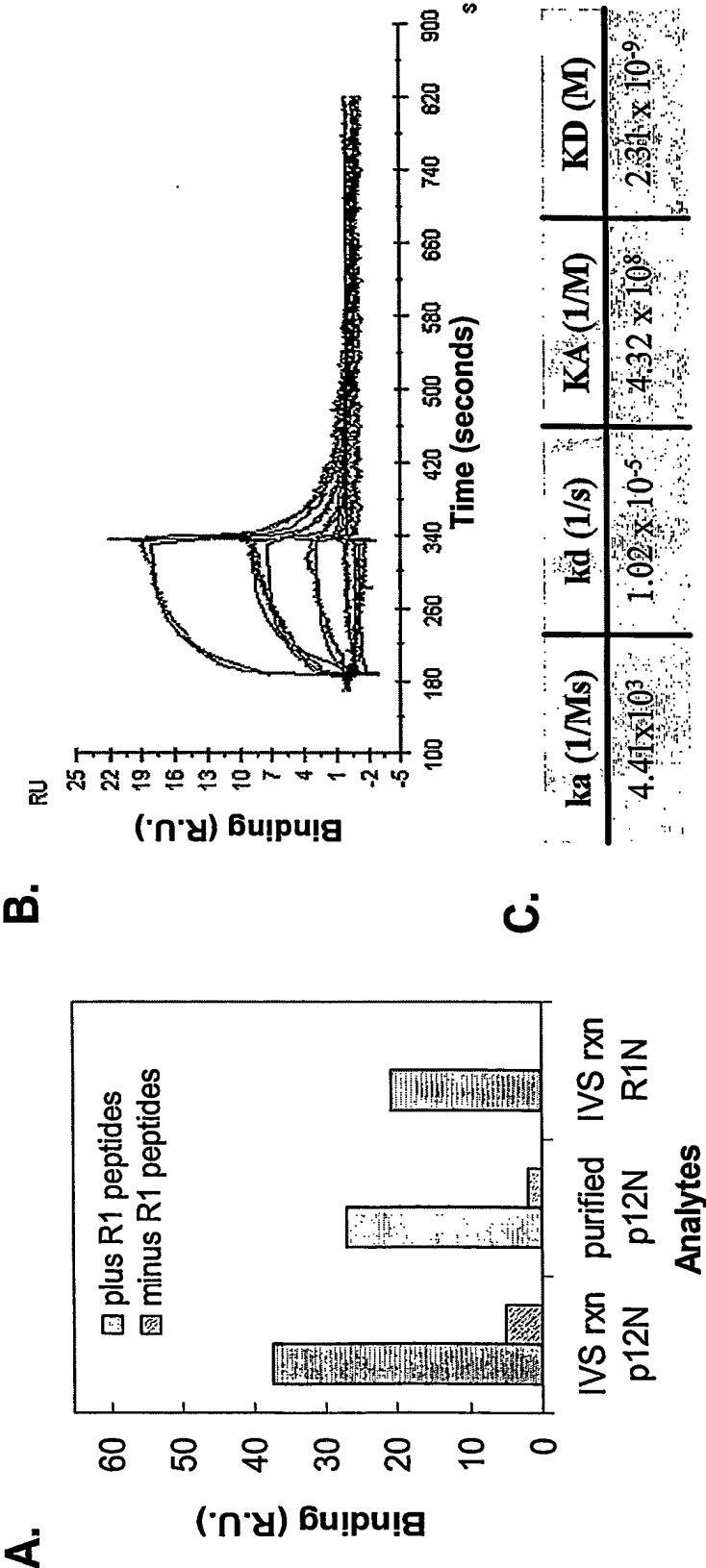


Figure 13.
A.

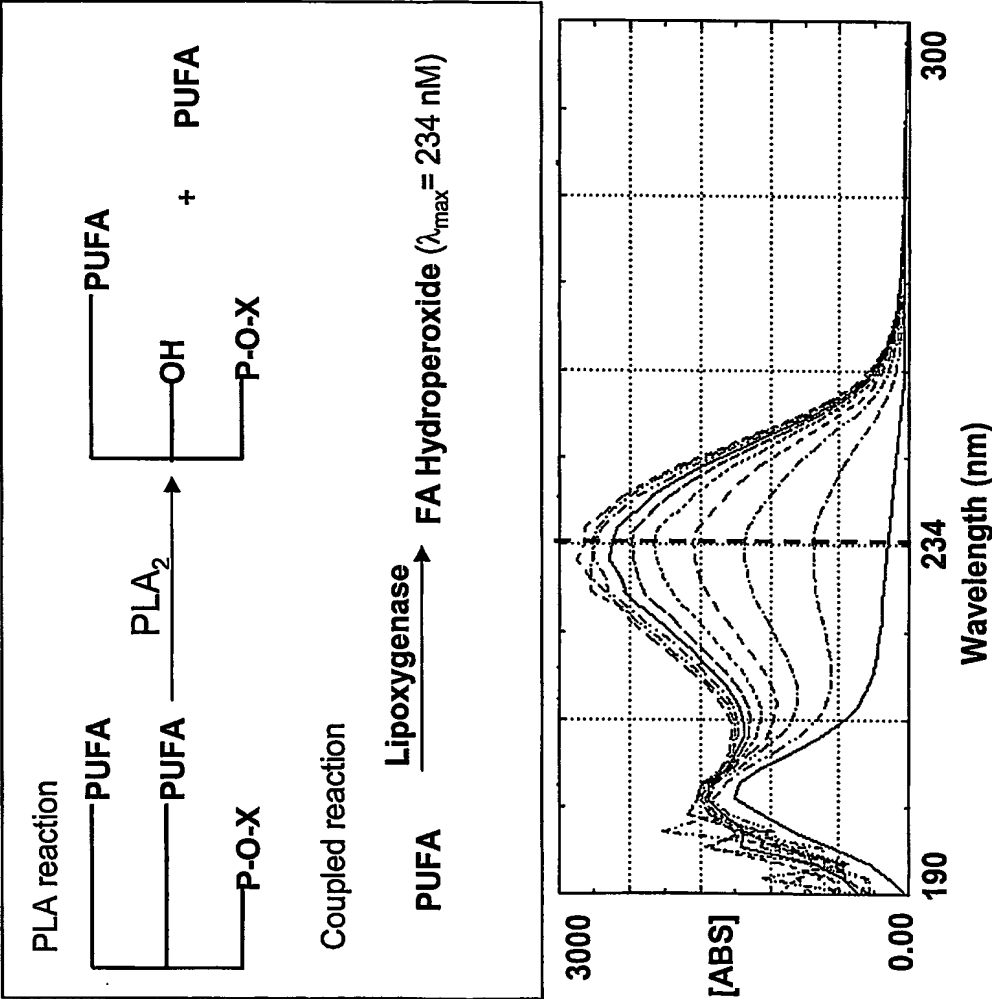


Figure 13.

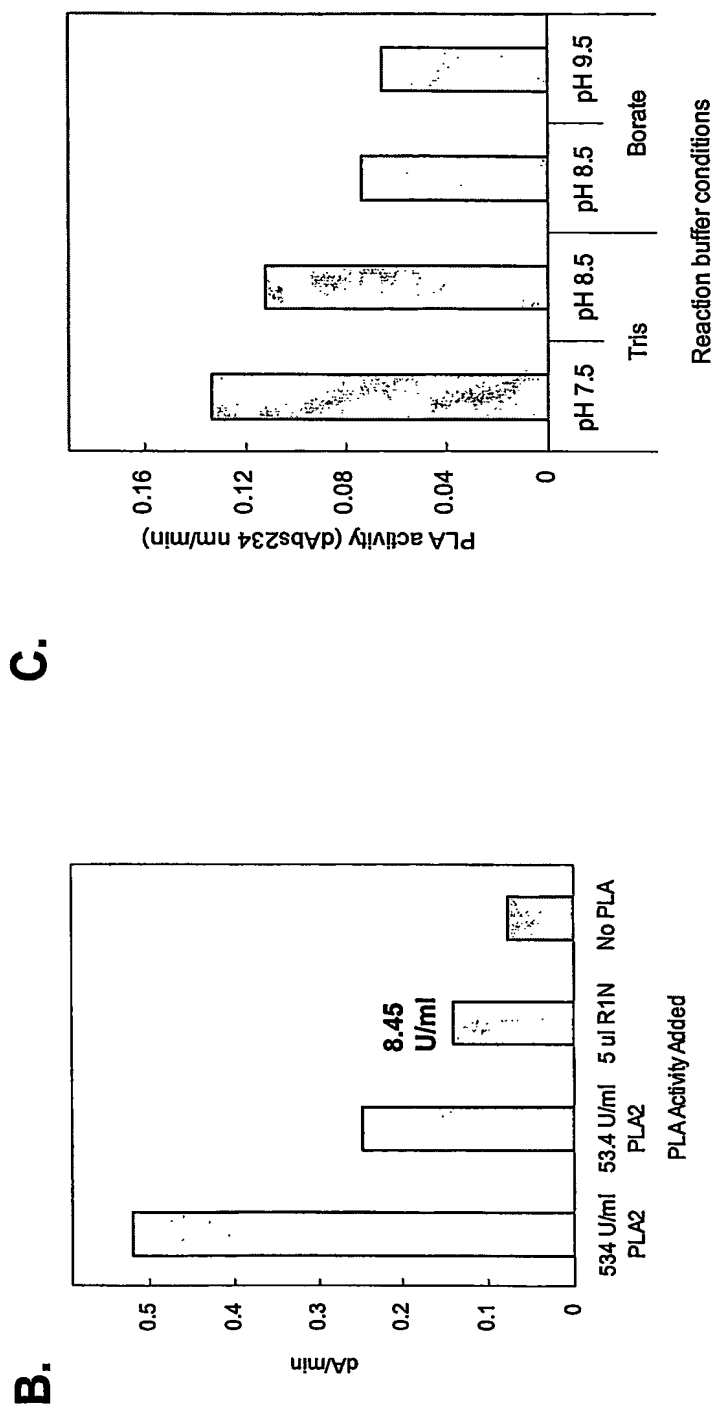


Figure 14.
A. COS-7 cells

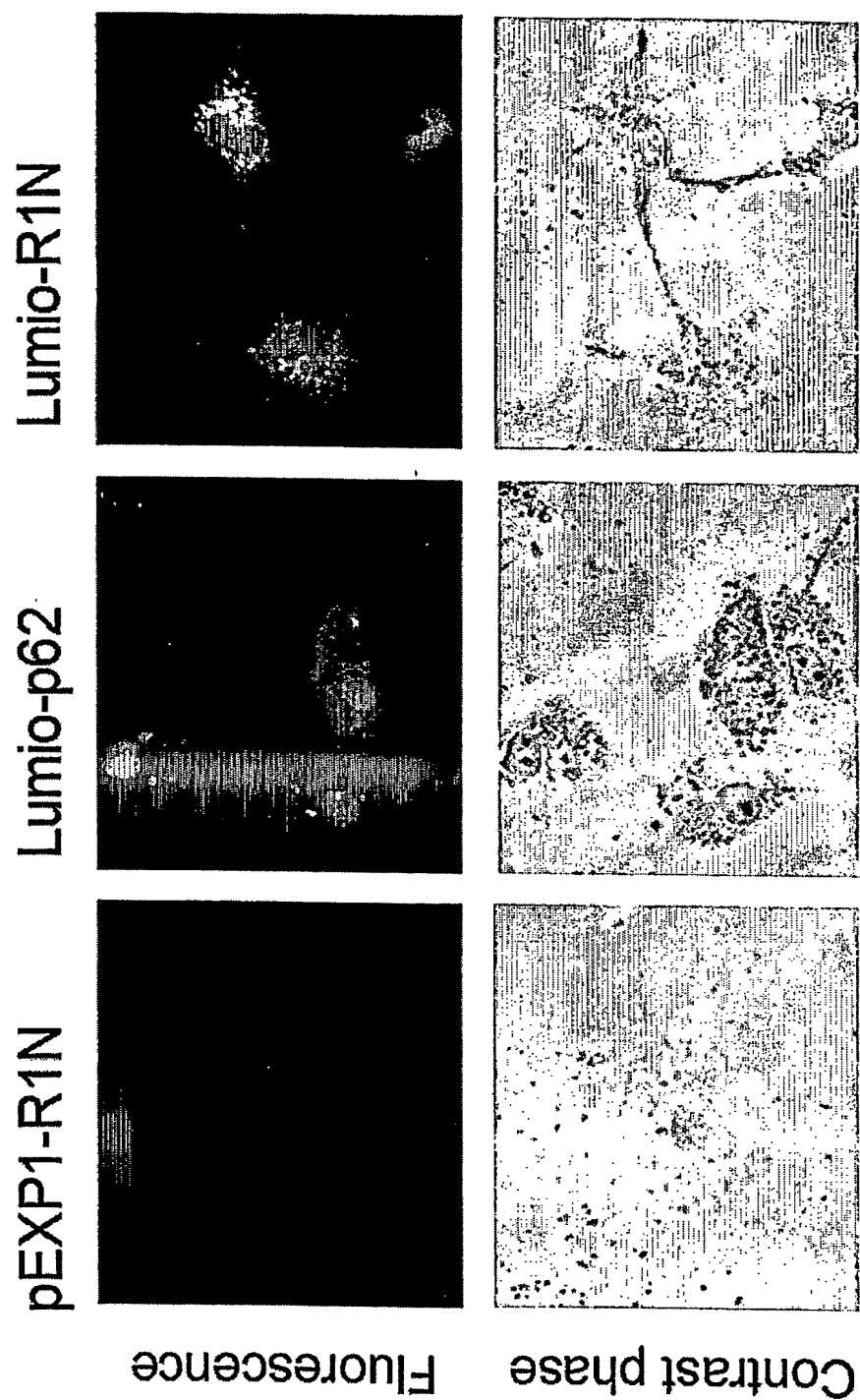


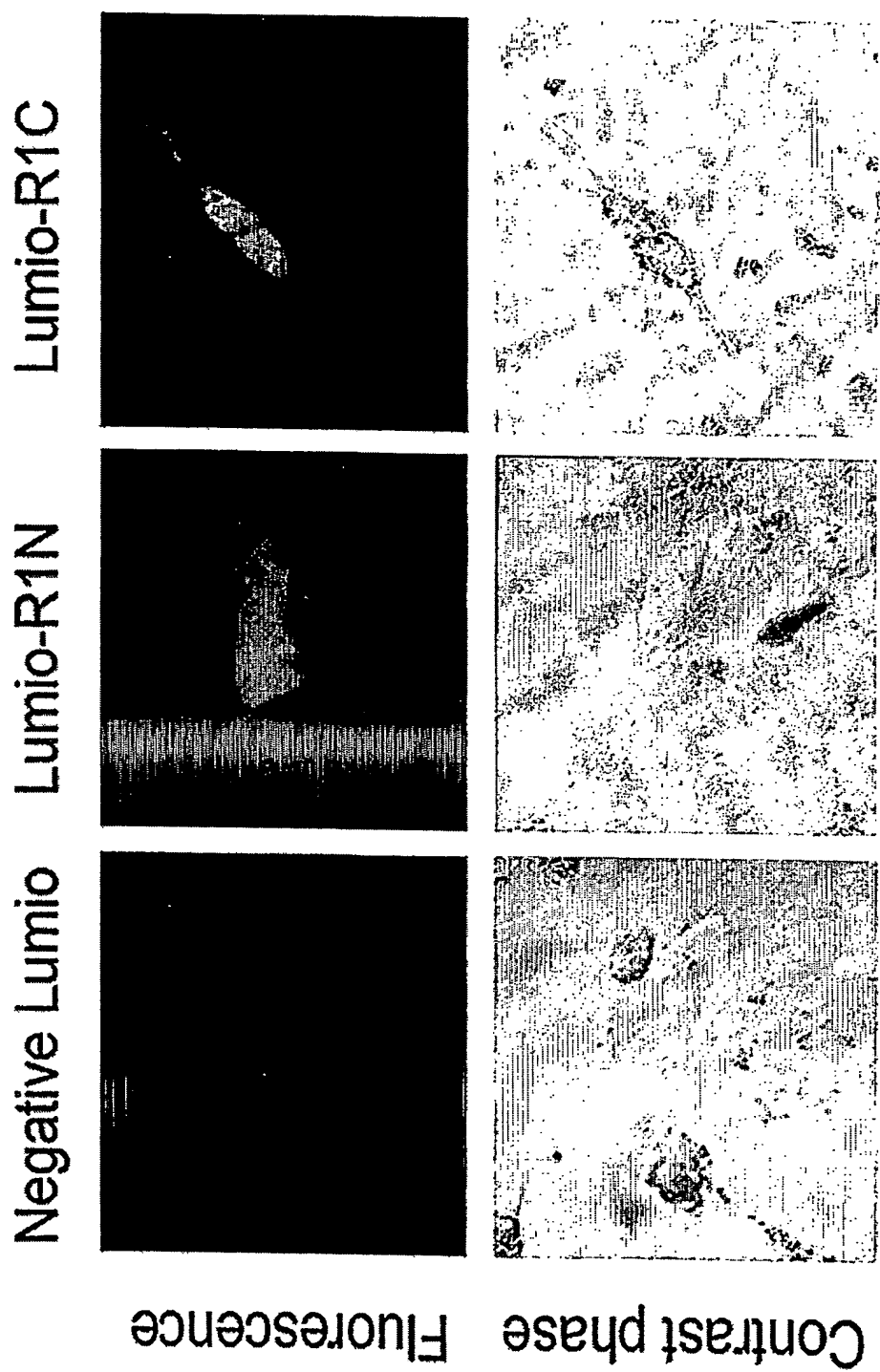
Figure 14.**B. Retinal ganglion RGC-5 cells**

Figure 15.

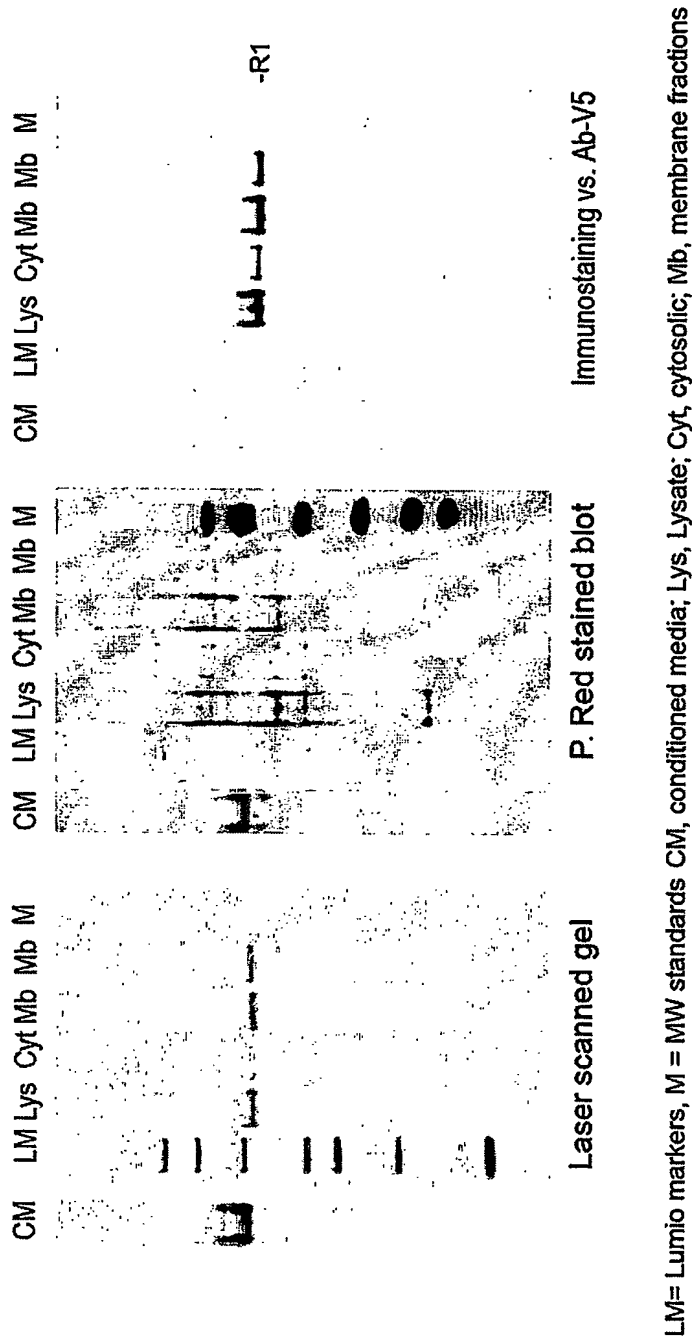


Figure 16.

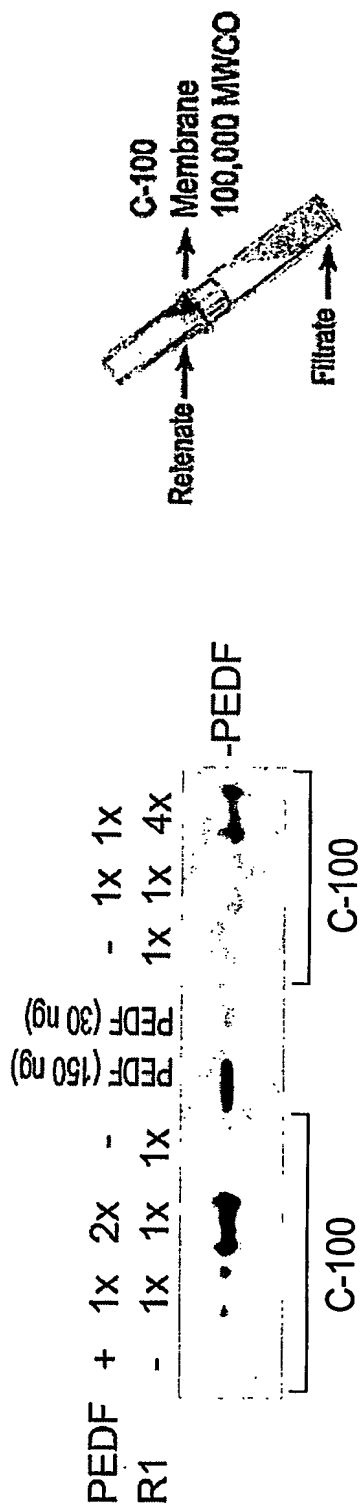


Figure 17.

A.

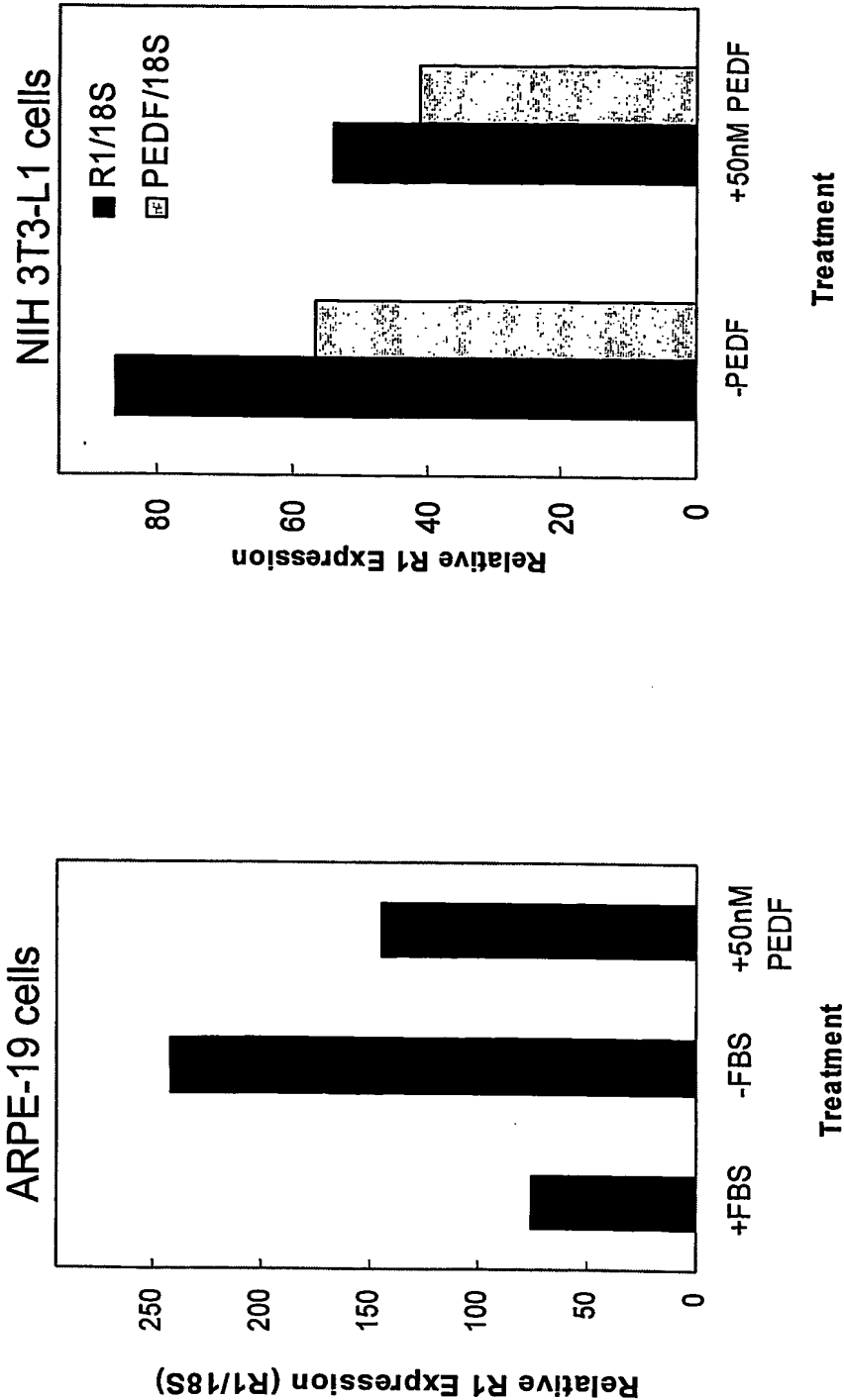


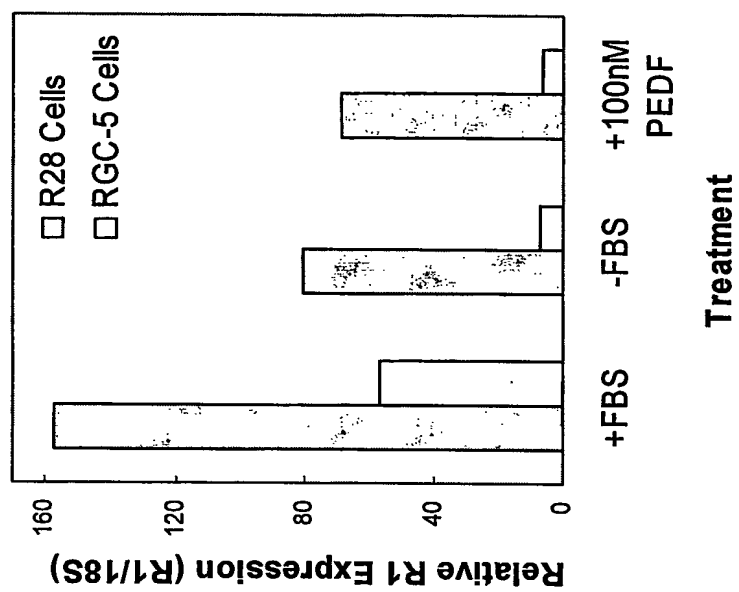
Figure 17.**B.**

Figure 17.

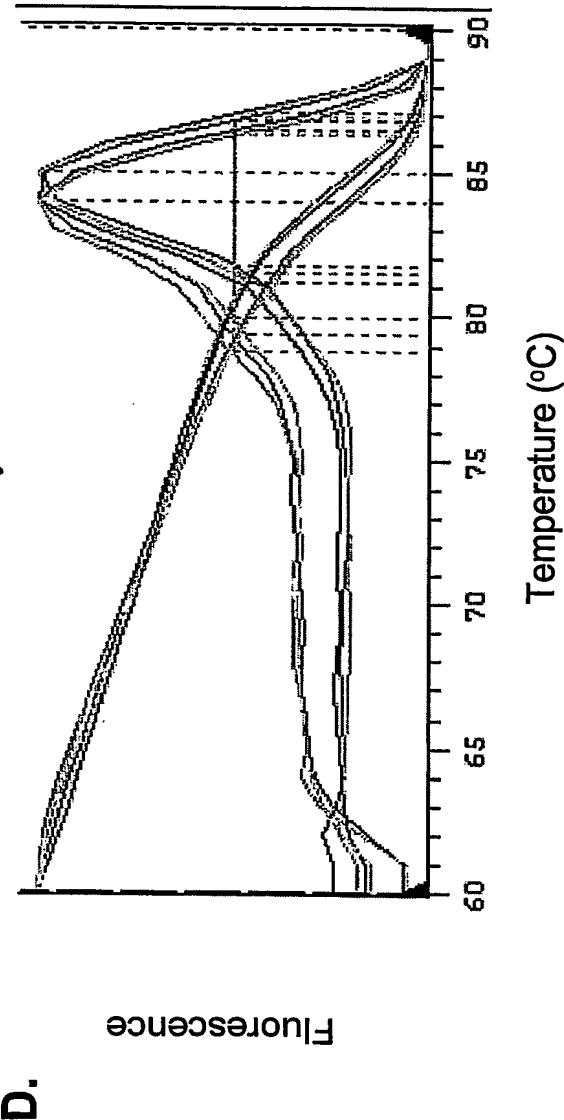
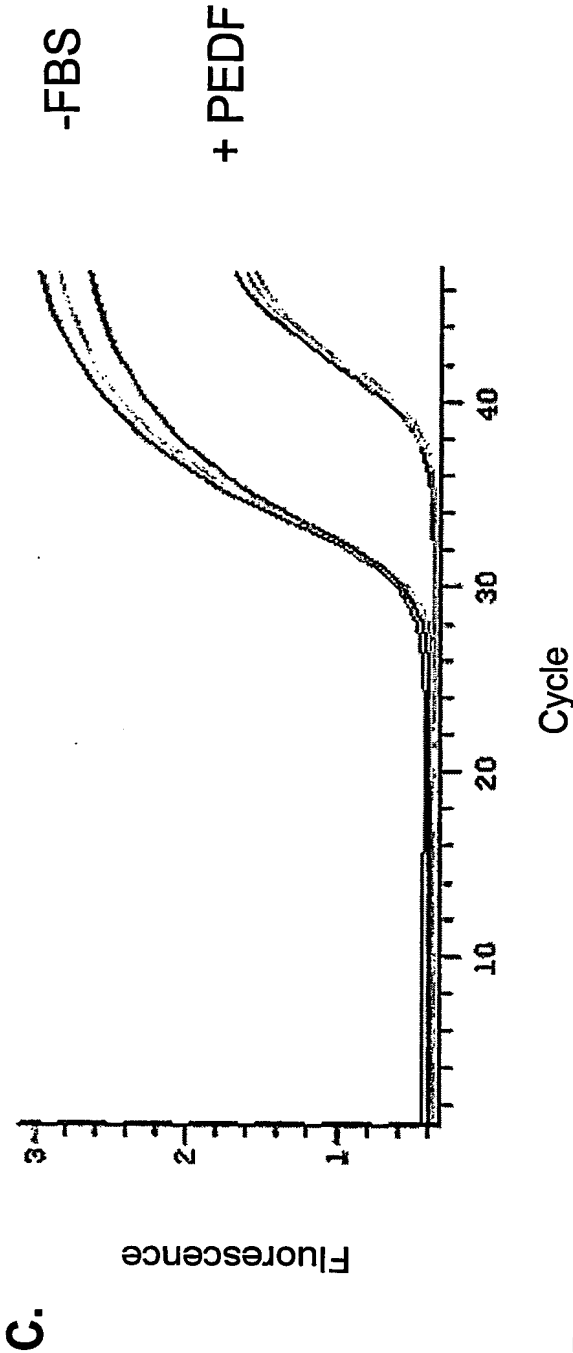


Figure 18.

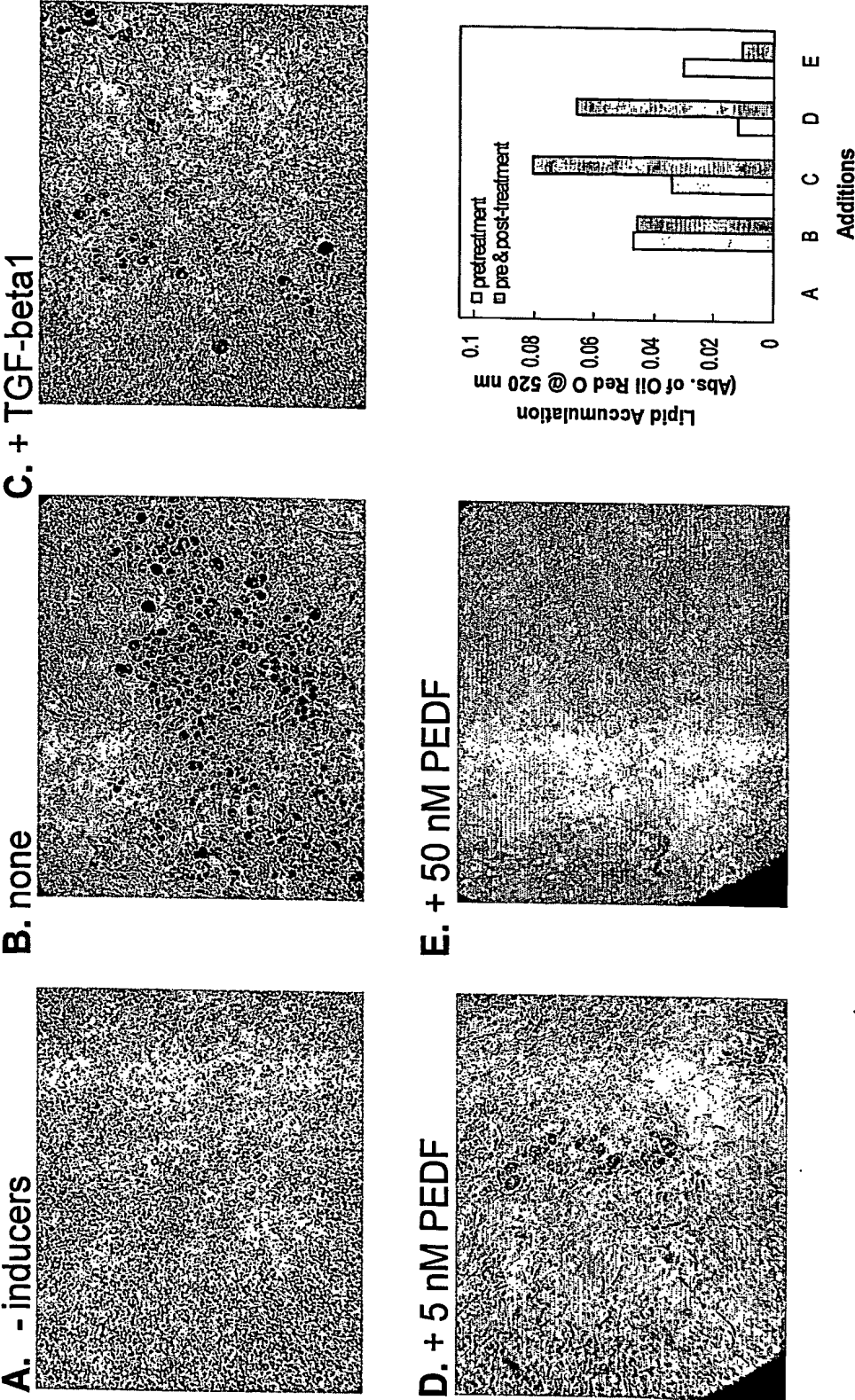


Figure 19.

CLUSTAL W (1.82) multiple sequence alignment

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gi|34861242|ref|XP_341961.1|      MFPRETKWNISFAGCGFLGVYHIGVASCLREHAPFLVANATHIYGASAGA 50
gi|16878147|gb|AAH17280.1|        MFPREKTWNISFAGCGFLGVYVGVASCLREHAPFLVANATHIYGASAGA 50
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gi|34861242|ref|XP_341961.1|      LTATALVTGACLGEAGANIEVSKEARKRFLGPLHPSFNLVKTIRGCLLK 100
gi|16878147|gb|AAH17280.1|        LTATALVTGVCCLGEAGAKFIEVSKEARKRFLGPLHPSFNLVKIIRSFLK 100
                                     *****:***** **
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gi|34861242|ref|XP_341961.1|      TLPADCHTRASGRGLGISLTRVSDGENVIISHFSSKDELIQANVCSTFIPV 150
gi|16878147|gb|AAH17280.1|        VLPADSHASGRGLGISLTRVSDGENVIISHFNSKDELIQANVCSTFIPV 150
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gi|34861242|ref|XP_341961.1|      YCGLIPPTLQGVRYVDGGISDNLPYELKNTITVSPFSGESDIPCQDSSST 200
gi|16878147|gb|AAH17280.1|        YCGLIPPSLQGVRYVDGGISDNLPYELKNTITVSPFSGESDIPCQDSSST 200
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gi|26327465|dbj|BAC27476.1|      NIHELVRTNTSIQFNLRNLYRLSKALFPPEPMVLREMCKQGYRDGLRFLR 250
gi|34861242|ref|XP_341961.1|      NIHELRTNTSIQFNLRNLYRLSKALFPPEPMVLREMCKQGYRDGLRFLR 250
gi|16878147|gb|AAH17280.1|        NIHELVRTNTSIQFNLRNLYRLSKALFPPEPLVLRMCKQGYRDGLRFLQ 250
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gi|26327465|dbj|BAC27476.1|      RNGLLNQPNPLALPPVVPQEEADAEAAVVEERAGEEDQLQPYRKDRILE 300
gi|34861242|ref|XP_341961.1|      RNGLLNQPNPLALPPVVPQEEADAEAAVTEERTGGED-----RILE 292
gi|16878147|gb|AAH17280.1|        RNGLLNRPNPLALPPARPHGPEDKDQAVESAQAEDYSQLP--GEDHILE 298
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gi|34861242|ref|XP_341961.1|      HLPARLNEALLEACVEPKDLMTTLSNMLPVRLATAMMVPTLPLESAVSF 342
gi|16878147|gb|AAH17280.1|        HLPARLNEALLEACVEPTDLLTTLSNMLPVRLATAMMVPTLPLESALSF 348
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gi|26327465|dbj|BAC27476.1|      TIRLLEWLDPVPEDIRWMKEQTGSICQYLVMAKRKLGDHLP SRLSEQVE 400
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gi|34861242|ref|XP_341961.1|      LRRQSLPSVPLSCATYSEALPNWVRNNSLGDALAKWEECQRQLLLGLF 442
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gi|34861242|ref|XP_341961.1|      CTNVAFPDALARMRAPAS--PTATDPATPDPSGLPPC----- 478
gi|16878147|gb|AAH17280.1|        CTNVAFPPEALARMRAPADPAPAPADPASFQHLQAGPAPLLSTPAPEARPV 498
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Figure 20. (1 of 4)

CLUSTAL W (1.82) multiple sequence alignment

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gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01-----
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gi|16878146|gb|BC017280.1|BC01-----
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gi|16878146|gb|BC017280.1|BC01-----
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ACGCTAATCAGCATGTTCCCAAGGGAGACCAAGTGAACATCTCGTTTCG 133
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gi|16878146|gb|BC017280.1|BC01-----
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gi|16878146|gb|BC017280.1|BC01-----
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Figure 20. (2 of 4)

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** * * * * * * * * * * * * * * * * * * * * *

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gi|26327464|dbj|AK031609.1|
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gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
TCGAATTCTAGAGCACCTGCCTGCCAGACTCAATGAGGCCCTGCTGGAGG 994
--GGATTCTAGAGCACCTGCCTGCCAGACTCAACGAGGCCCTGCTGGAGG 1009
TCACATCTGGAGCACCTGCCCGCCGCTCAATGAGGCCCTGCTGGAGG 1142
** * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
CCTGTGTGGAACCAAGGACCTGATGACCACCTTTCCAACATGCTACCA 1044
CCTGTGTGGAACCGAAAGACCTGATGACCACCTTTCCAACATGCTGCCA 1059
CCTGCGTGGAGCCACGGACCTGCTGACCACCTTCCAACATGCTGCCT 1192
**** * * * * * * * * * * * * * * * * *
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CTGTGGAATGAGGACATAGGACCCCTGCACAGCTGCAAGTGGGCTTTCGAT 1684

CTGCGCAGTGAGATGAGGGGACTCACAGTTGCCAAGAG-GGGTCTTTGCC 1822

Figure 20. (4 of 4)

gi 26327464 dbj AK031609.1	GTGAAACCTTTTACCAGCCACTCACTATGCTACTCCTGGTGGGGAGGGAT	1734
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	GTGGGCCCCCTCGCCAGCCACTCACCA-GCTGCATGCACTGAGAGGGGAG	1871
gi 26327464 dbj AK031609.1	GGGGAGTCGCCCTCCCCGGAGCCACAGAGCCCTCCCCCGTCACGTC--	1782
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	GTTTCCACACCCCTCCCTGGGCCGCTGAGGCCCGCGCACCTGTGCCTT	1921
gi 26327464 dbj AK031609.1	ACCTGTGCCTTACTCCTGCCACCA--CCTTTTCAGTGCAGGGTCAGTCT	1830
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	AATCTTCCCTCCCTGTGCTGCCCGAGCACCTCCCCGCCCTTTACTCC	1971
gi 26327464 dbj AK031609.1	TAAGAACTCCACATCTGCTGCTGC-TCCCTGGTGTCCAAGTTTCCTTGCA	1879
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	TGAGAACTTTGCAGCTGCCCTTCCCTCCCGTTTTTCATGGCCTGCTGAA	2021
gi 26327464 dbj AK031609.1	GA--GTGTGTGAAGAATTATTTATTTTTCGCAAAGCAGATCTAATAAAAG	1927
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	ATATGTGTGTGAAGAATTATTTATTTTCGCAAAGCACATGTAATAAATG	2071
gi 26327464 dbj AK031609.1	CCACAGCTCAGCTTCTGCCTTCCTCACTTCTGCATGCT-----	1965
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	CTGCAGCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2121
gi 26327464 dbj AK031609.1	-	
gi 34861241 ref XM_341960.1	-	
gi 16878146 gb BC017280.1 BC01	A	2122